AMENDMENTS

Please amend the claims as follows:

1.–2. (Cancelled)

3. (Previously Presented) The method of claim 20, wherein said DNA is non-genomic DNA.

4. (Previously Presented) The method of claim 20, wherein said DNA is cDNA.

5.–19. (Cancelled)

20. (Previously Presented) A method of subjecting a DNA molecule to a DNA synthesis reaction, comprising the steps of:

a) obtaining a DNA molecule having a first linker sequence positioned at one end of the DNA molecule and a second linker sequence, different from said first linker sequence, positioned at the other end of the DNA molecule; and

b) subjecting said DNA to a DNA synthesis reaction with a primer set comprising:

i) a first primer, wherein the 5' sequence of said primer is complementary to said first linker sequence and the 3' sequence of said primer comprises a specificity region; and

ii) a second primer, wherein the 5' sequence of said primer is complementary to said second linker sequence and the 3' sequence of said primer comprises a specificity region

wherein both the specificity regions of both the first and second primers comprise random sequences.

21. (Previously Presented) The method of claim 85, wherein said amplification is performed with an array of combinations of alternate amplification primers.

22. (Cancelled)

23. (Previously Presented) The method of claim 85, further comprising, identifying the amplified DNA.

24. (Original) The method of claim 23, wherein said identification is based upon length.

25. (Original) The method of claim 23, wherein said identification is performed by a computer program.

26. (Original) The method of claim 21, wherein said array of amplifications is performed in a multi-well plate.

27. (Original) The method of claim 20, wherein the specificity region of the primers of the first primer set is 3,4,5,6,7 or 8 base pairs long.

28. (Original) The method of claim 20, wherein the specificity region of the primers of the second primer set is 3,4,5,6,7 or 8 base pairs long.

29. (Previously Presented) The method of claim 85, wherein said amplification comprises polymerase chain reaction, nucleic acid sequence based amplification, transcription mediated amplification, strand displacement amplification or ligase chain reaction.

30. – 35. (Cancelled)

36. (Previously Presented) The method of claim 85, wherein a label is incorporated into said amplified DNA.

37. (Original) The method of claim 36, wherein said label is incorporated by means of a labeled primer.

38. (Original) The method of claim 36, further comprising, partial nucleotide sequence identification of the amplified products by the identity of the label.

39. (Original) The method of claim 36, wherein said label is a chromophore.

40. (Original) The method of claim 36, wherein said label is a fluorophore.

41. (Original) The method of claim 36, wherein said label is an affinity label.

42. (Original) The method of claim 36, wherein said label is a dye.

43. (Original) The method of claim 37, wherein the 5' end of said primer comprises an amino moiety and a flurophore is covalently attached by the reaction of a succinimido ester of the flurophore to the 5' amino-modified primer.

44. (Original) The method of claim 40, wherein said fluorophore is Alexa 350, Alexa 430, AMCA, BODIPY 630/650, BODIPY 650/665, BODIPY-FL, BODIPY-R6G, BODIPY-TMR, BODIPY-TRX, Cascade Blue, Cy2, Cy3, Cy5,6-FAM, Fluorescein, HEX, 6-JOE, Oregon Green 488, Oregon Green 500, Oregon Green 514, Pacific Blue, REG, Rhodamine Green, Rhodamine Red, ROX, TAMRA, TET, Tetramethylrhodamine, and Texas Red.

45. (Previously Presented) The method of claim 20, wherein the products of said DNA synthesis reaction are analyzed.

46. (Previously Presented) The method of claim 45, wherein said analysis of products is by polyacrylamide gel electrophoresis.

47. (Previously Presented) The method of claim 45,wherein said analysis of products is by capillary gel electrophoresis.

48. (Previously Presented) The method of claim 45, wherein said analysis of products is by mass spectrophotometry.

49. (Previously Presented) The method of claim 45, wherein said analysis of products is by energy transfer.

50. (Previously Presented) The method of claim 45, wherein said analysis of products is by a filtration and extraction device.

51. (Previously Presented) The method of claim 45, wherein said analysis of products is by the use of interlaced lasers and multiple fluorescent measurements.

52. (Previously Presented) The method of claim 45, wherein said analysis of products comprises quantifying amplification products.

53. (Previously Presented) The method of claim 52, wherein said quantifying is by measuring the ratio of each product to a co-amplified reference-gene.

54. (Previously Presented) The method of claim 52, wherein said quantifying is by measuring the ratio of each product to a panel of reference-genes.

55. (Previously Presented) The method of claim 52, wherein said analysis of products is by Real-Time PCR.

56. (Previously Presented) The method of claim 45, wherein said analysis of products is performed in a multi-well plate.

57. (Previously Presented) The method of claim 45, wherein said analysis of products is performed on a membrane.

58. (Previously Presented) The method of claim 45, wherein said analysis of products is performed on a solid matrice.

59. (Original) The method of claim 58, wherein said solid matrice is a DNA chip.

60. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a different cell or tissue.

61. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cancerous cell or tissue.

62. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a pharmaceutical compound.

63. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a teratogenic compound.

64. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a carcinogenic compound.

65. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a toxic compound.

66. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a biological response modifier.

67. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a hormone, a hormone agonist or a hormone antagonist.

68. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a cytokine.

69. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a growth factor.

70. (Previously Presented) The method of claim 20, performed on DNA derived from a normal cell or tissue and on the DNA derived from a cell or tissue treated with the ligand of a known biological receptor.

71. (Previously Presented) The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue type obtained from different species.

72. (Previously Presented) The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue type obtained from different organisms.

73. (Previously Presented) The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue at different stages of development.

74. (Previously Presented) The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a normal cell or tissue and derived from a cell or tissue that is diseased.

75. (Previously Presented) The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue cultured in vitro under different conditions.

76. (Previously Presented) The method of claim 20, performed on the DNA derived from a cell or tissue from two organisms of the same species with a known genetic difference.

77.–84. (Cancelled)

85. (Previously Presented) The method of claim 20, wherein the first and second primers are employed to amplify the DNA molecule.

86. (Previously Presented) The method of claim 20, wherein the first and second primers are employed to sequence the DNA molecule.

87. (Currently amended) A pair of primer molecules wherein both members of the pair comprise (a) a predetermined 5' sequence that incorporates a sequence that anneals to a predetermined linker sequence and (b) a random 3' terminal specificity region of from 3 to 8 nucleotides in length, the specificity region defined as one of all possible sequence combinations of A, T, G and C, and wherein each member of the pair anneals to a different predetermined linker sequence from the other member of the pair.

88. (Currently amended) A population of paired primer molecules, the primer molecule pairs having (a) a predetermined 5' sequence that incorporates a sequence that anneals to a predetermined linker sequence and (b) a random 3' terminal specificity region of from 3 to 8

nucleotides in length, the population of primer molecules having specificity regions collectively reflecting all possible sequence combinations of A, T, G and C, and wherein each member of the pair anneals to a different predetermined linker sequence from the other member of the pair..